



Figure 3. Principal Components Analysis of the soil prokaryote community obtained by sequencing the 16S rRNA gene from soil samples collected from a) full-season soybean (June 2015) b) winter wheat (May 2016) and c) corn (June 2017). The community composition did not differ significantly between treatments in full-season soybean (PERMANOVA  $P=0.728$ ,  $R^2=0.083$ ), winter wheat (PERMANOVA  $P=0.208$ ,  $R^2=0.108$ ), or corn (PERMANOVA  $P=0.317$ ,  $R^2=0.104$ ).